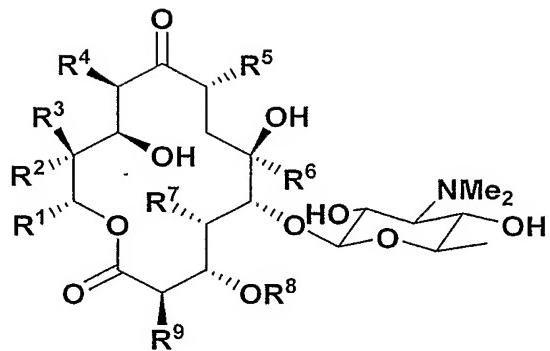
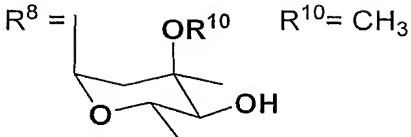


Figure 1A

5-O-dedesosaminyl-5-O-mycaminosyl-erythromycin B

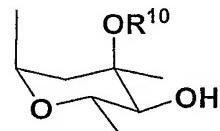
$R^1 = C_2H_5$ $R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3$ $R^3 = -H$ $R^8 =$



5-O-dedesosaminyl-5-O-mycaminosyl-erythromycin A

$R^1 = C_2H_5$ $R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3$ $R^3 = -OH$ $R^8 =$

$R^{10} = CH_3$



5-O-dedesosaminyl-5-O-mycaminosyl-erythromycin C

$R^1 = C_2H_5$ $R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3$ $R^3 = -OH$ $R^8 =$

$R^{10} = H$

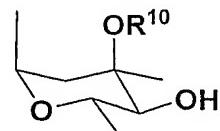
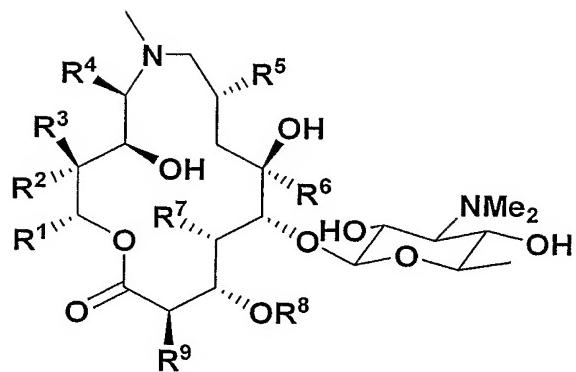


Figure 1B

5-O-dedesosaminyl-5-O-mycaminosyl-azithromycin

$R^1 = C_2H_5$ $R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3$ $R^3 = -OH$ $R^8 =$

CH_3

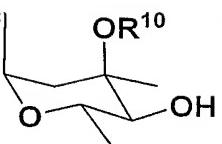


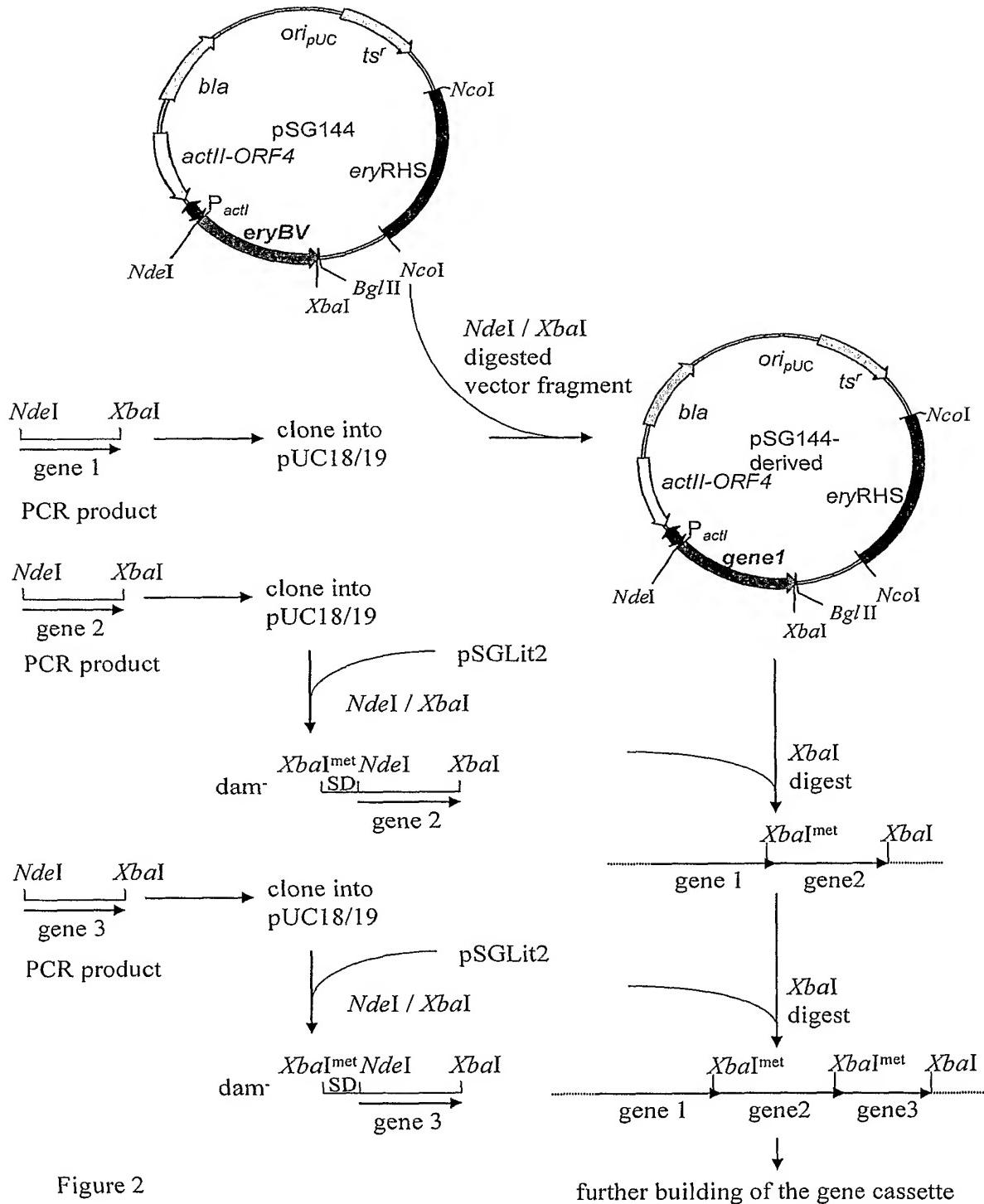
Figure 2

Figure 2

Figure 3

TylA1.pep x u08223.em_pro2

5

1 MNDRPRRAMKGIILAGGSGTRLRPLTGTLSKQLLPVYDKPMIYYPLSVL M 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MNDRPRRAMKGIILAGGSGTRLRPLTGTLSKQLLPVYDKPMIYYPLSVL M 50
10
51 LAGIREIQIISSSKDHLDFRSLLGEGDRLGLSISYAEQREPRGIAEAFL I 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 LAGIREIQIISSSKDHLDFRSLLGEGDRLGLSISYAEQREPRGIAEAFL I 100
15
101 GARHIGGDDAALILGDNVFHGPFGSSVLTGTVARLDGCELFGYPVKDAHR 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 GARHIGGDDAALILGDNVFHGPFGSSVLTGTVARLDGCELFGYPVKDAHR 150
20
151 YGVGEIDSGGRLLSLEEKPRRPRSNLAVTGLYLYTNDVVEIARTISPSAR 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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25
201 GELEITDVNKVYLEQGRARLTTELGRGFAWLDMGTHDSLLQAGQYVQLLEQ 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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30
251 RQGERIACIEEIAMRMGFISAEQCYRLGQELRSSSYGSYIIDVAMRGAAA 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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299 DSRAQ 303

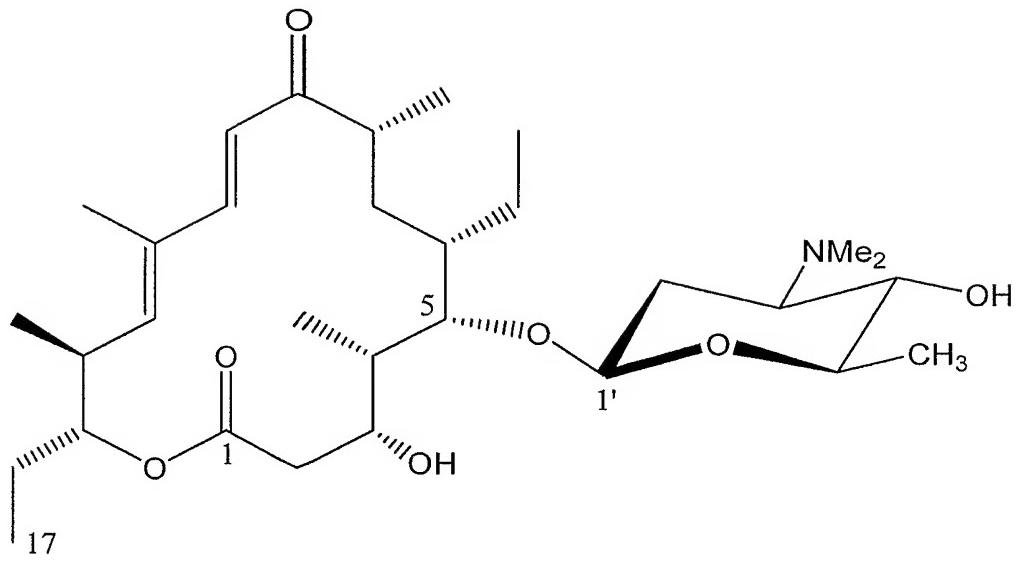
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Figure 4

TylAII.pep x u08223.em_pro2

5

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1 MRVLVTGGAGFIGSHFTGQLLTGAYPDLGATRTVVL~~D~~KLTYAGNPANLEH 50
0 51 VAGHPDLEFVRGDIADQALVRRLMEGVGLVVHFAAEHVDRSIESSEAFV 100
51 VAGHPDLEFVRGDIADHGWWRRILMEGVGLVVHFAAEHVDRSIESSEAFV 100
5 101 RTNVEGTRVLLQAAVDAGVGRFVHISTDEVYGSIAEGSWPEDHPLAPNSP 150
101 RTNVEGTRVLLQAAVDAGVGRFVHISTDEVYGSIAEGSWPEDHPVAPNSP 150
0 151 YAATKAASDLLALAYHRTYGLDVRVTRCSNNYGPRQYPEKAVPLFTTNLL 200
151 YAATKAASDLLALAYHRTYGLDVRVTRCSNNYGPRQYPEKAVPLFTTNLL 200
5 201 DGLPVPLYGDGGNTREWLHVDDHCRGVALVAAGGRPGVIYNIGGGTELTN 250
201 DGLPVPLYGDGGNTREWLHVDDHCRGVALVGAGGRPGVIYNIGGGTELTN 250
0 251 AELTDRILCGADRSAVRRVADRPGHDRRYSDTTKIREELGYAPRTGI 300
251 AELTDRILCGADRSALRRVADRPGHDRRYSDTTKIREELGYAPRTGI 300
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301 TEGLAGTVAWYRDNRRAWWEPLKRSPGGRELER 333

Figure 5

5

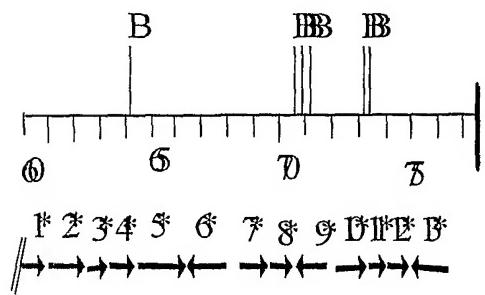
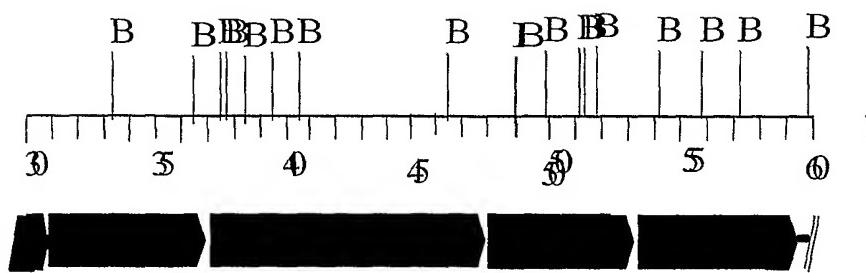
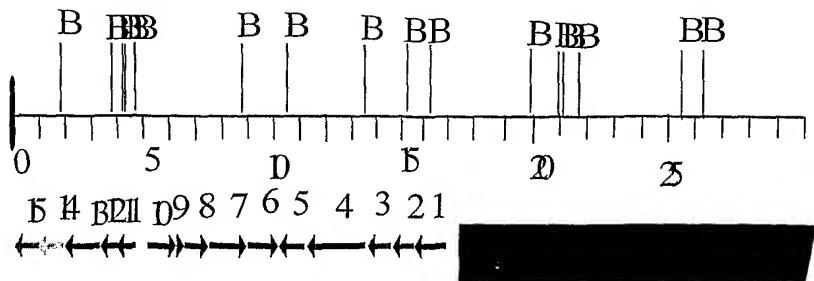
Figure 6

Figure 7

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51 51 GTGCAGGGCC GCGATCACCT TGTCTGTAC GTCGGGCGCG AGCCCCGGGT
10 101 ACATCGGCAG CGAGAAGATC TCGTCCGCCA GCCGCTCCGT CACCGGCAGC
15 151 GAGCCCTTGG CGTACCCCAG GTGCGCGAAG CCCGTATGG TGTGCACGGG
20 201 CCACGGGTAA CTGATGTTGA GCGAGATCCC GTACGACTTG AGCCCTCGA
25 251 TGATGTCGTC CCGGCGCGGG TGGCGGACGA CGTACACGTA ATACACGTGG
30 301 TCGTTGCCCT CGGTGACGGA CGGCAGCACC AGGCCGCCGG GGCCCCTCAG
20 351 GTTCGCGAGT CCTTCGGCGT AACGCCGGC GACCGCGCAG CGGCCCTCGA
40 401 TGTAGCGGTC GAGGCGGGTG AGCTTGCAGC GCAGGATCTC CGCCTGCACC
45 451 TCGTCGAGCC GGCTGTTGTG GCCGGCGTC TGCACGACGT AGTACACGTC
25 501 CTCCATGCCG TAGTAGCGCA GCCGGCGCAG CGCACGGTCG ACGTCCCGT
50 551 CGTCGGTCAG CACGGCCCCG CCGTCGCCGT ACGCACCGAG GACCTTCGTC
30 601 GGGTAGAACG AGAAGGCGGC GGCGTCGCC AGCGTGCCGG CCAGCTCGCC
651 651 GTGGTGGCGG GCACCGTGCG CCTGGCGCA GTCCTCCAGC ACCACCAGGC
701 701 CGTGCTGCTC GGCCAGGGCG CGCAAGGGCG CCATGTCGAC GCACTGCCCG
35 751 TACAGGTGCA CCGGCAGCAG GGCTTCGTG CGCGGGGTGA TGACGTCCGC
801 801 GACCTGGTCG GTGTCCATGA GGTGGTCCTC GGCGCGGACG TCGACGAAGA
40 851 CGGGCGTGGC ACCGGTGCCG TCGATGCCA CCACCGTCGG CGCGGCCGTG
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951 951 ACCCAGCTT ACGGCGTTGG TGCCGTTGTC GACACCGCCG CAGTGGCGCA
45 1001 GGCCGTGGTA GTCCCGCAAC TCCTTCTCGA ACCCGTCCAC GCTGGGGCCG
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50 1101 CGCGCGTTCG TTCTGGTATT CCGCCAGGTA GTCCCAGACG TAGGTAGTCA
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1301 1301 AGCCAGTCCT CCCGGTGCCCC GGGAGCCCGG CCCGGAGCCG GGCGCTCCAC
60 1351 CACCCGCGCC GGAATGCCGC TCGCCTCGAT GAACAGGCG ACCAGGTCGC
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1451 GGTGCCGGGG CGGCAGGCCAC GACGGCGTCG GCCACGTCCC GCACATCGAC
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1701 GCTTGCTCCT GCCGTACGCC GTGTCCGGC GCGGTACGGC GTCGGCGCCC
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25 2001 GGTACGGCAT CGGCTCCTCG GGCGGGCGGC GGCCCACACAC CACCACGTCA
2051 CGGGCCCCGGC CGGCGAACGC CGCGCACACA TGCCGGCCGA CGTACCCGGC
2101 GCCGCCAGG ACCACGACGC TGCCACTGCC ACTGCCCGCGC GGCATCGGAT
30 2151 CGTTCACCAT

Figure 8

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 10 11451 ATCACGTAGC GGTTCTGGC GTGGAAGAAC CGCCCGCCCT CCTCGGACTG
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 15 11551 GGTACGGCGG GCCGGGCAGC CCCCAGGAC CGGTGTGCTC CTGTGGCCGG
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 11651 CCGTGCCCCG ACGAGCGCGT GCAGCACGCC GTCGACGGAC TTGACCAGCA
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5 12801 GGCAGGGACGG GGCCGGTGCT CGTGTCCCGC GCGGTACGCG GTGGGACGGT
12851 CCCGGTGGCC GTGTCCCGG TGGCCGTGCC GGCAGGGCG TCGCCGATGG
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5 14351 CCTCGCGCCA CGACCCCTCG GCGATCGAGC CGTACACCTC GTCCGTGGAG
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15751 GTCTTCGTCA T

Figure 9

| | | |
|----|--|---|
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| 10 | 59801 CAACTGACCC GCGCAGCCCA GTGGTTCGCG GGAACCCAGG ACGACCCGTA | |
| | 59851 CGCGCTCGTC CTGCGCGCCG AGGCCACCGA CCCGGCCCCG TACGAGGAGC | |
| | 59901 GGATCCGGGC CCACGGGCCG CTCTTCCGCA GCGACCTGCT CGACACCTGG | |
| 15 | 59951 60001 GTCACGGCGA GCAGGGCCGT CGCCGACGAA GTGATCACCT CACCCGCCTT | |
| | 60001 CGACGGGCTC ACGGCCGACG GGCAGGCCCG CGGCGCGCGG GAACTGCCGC | |
| 20 | 60051 60101 TGTCCGGCAC CGCGCTCGAC GCGGACCGCG CCACATGCGC ACGGTTCGGG | |
| | 60101 GCCCTCACCG CCTGGGGCGG GCCGCTGCTG CGGCGGCCGC ACGAGCGGGC | |
| | 60151 60201 GCTGCGCGAG TCCGCCGAAC GGCAGGCCCA CACACTCCTC GACGGGGCGG | |
| 25 | 60201 AGGCCGCCCT GGCCGCCGAC GGCACCGTCG ACCTCGTCGA CGCGTACGCC | |
| | 60251 60301 CGCAGGCTCC CGCGCTGGT CCTCCGCGAA CAGCTCGCG TGCCGGAGGA | |
| 30 | 60301 GGCAGGCCACC GCCTTCGAGG ACGCGCTGGC CGGCTGCCGC CGCACCCCTGG | |
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| 35 | 60451 60501 GGCCGGCCGG GCCCCCGACG CCGTCGCCGC CGCCCGCACC CTGGCGTCG | |
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| | 60601 GGCCGCCCG CGTGACCGAAA CGCTCGTGT CGCCCGCCCG GTCCGCCTGG | |
| | 60651 60701 AGCGGCGGGT CGCCCGCGAG GACACGGACA TCGCCGGCA GCGCCTCCCC | |
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| 50 | 60801 CCCGTACCTC CGCCCCCTCC GTCCCCTCAG CCCCCTTCGA CCTCACACGG | |
| | 60851 60901 CCCGTGGCCG CGCCCGGGCC GTTCGGGCTC CCCGGCGACC TGCACCTCCG | |
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| 55 | 60951 61001 TGGCCGCACG GCTCCCCGGT CTGCGCGCCG CGGGGCCGGC CGTGC | |
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| | 61051 61101 CGGGACGGCC CGTGACCTGC CCGCCACCGC ACCGCAGAAC TGAGGAGGGA | |
| 60 | 61101 GTGCCCCGAT GCGTATCCTG CTGACGTCGT TCGCGCACAA CACGCAC | |
| | 61151 TACCGACCGC CGGACACGCC CGCCTCCCCG TCGCCGTGCG | |

61201 TACAACCTGG TCCCCCTCGG CTGGGGCCTG CGCGCCGCCG GGCACGACGT
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62501 ACCAGGGAAA GGGCAAGGAC TACCGGGCGG AGGCCGAGGA GCTGGCCGCG
55 62551 CTTGTCACCC AGCGCCGCC CGGGGCCCGC TCCCTCCTCG ACGTGGCCTG
62601 CGGAACGGGG ATGCACCTGC GGCACCTCGG CGACCTCTTC GAGGAGGTGG
60 62651 CGGGGGTGG AATGTCCCCC GACATGCTGG CCATCGCGCA CGGGCGCAAC

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62701 CCGGAGGCCG GCATCCACCG GGGGGACATG CGGGACTTCG CCCTCGGCCG
62751 CCGCTTCGAC GCCGTGATCT GCATGTTCA G TTCCATCGGG CACATGCGCG
5 62801 ACCAGCGGGA ACTGGACGCG GCGATCGGCC GGTTCGCCGC GCACCTGCCG
62851 TCCGGCGGGG TCGTGATCGT CGATCCCTGG TGTTCCCAG AGACGTTCAC
10 62901 ACCGGGGTAC GTGGCGCGA GCCTCGTCGA GGCGAGGGC CGCACCATCG
62951 CGCGCTTCTC CCACTCCGCG CTCGAGGACG GCGCGACCCG GATCGATGTG
63001 GACTACCTCG TCGGCGTGCC GGGGGAGGGG GTGCGGCAC TGAAGGAGAC
15 63051 CCATCGGATC ACGCTTTCG GGC GTGCGCA GTACGAGGCG GCCTTCACCG
63101 CGGCAGGGAT GTCCGTCGAG TACCTCCGC ACGCCGCCAC CGACCGCGGA
20 63151 CTCTTCGTCG GCGTCCAGGC CTGA

Figure 10

1 MKGIILAGGS GTRLRPLTGA LSKQLLPVYD KPMIYYPLSV LMLAGIRDIQ
5
51 IITSKTHLEM FRSLLGDGSR IGISVGYAEQ EEPRGIAEAF LIGEEHIGDD
101 PVALILGDNV FHGPGFSSVL ASTAARLDGC ELFGVVKDP RRYGVGEVDA
0
151 EGRLVSLEEK PEKPRSHLAV TGLYFYDNGV VDIARRLTPS PRGELEITDV
201 NKVYLEQGRA RMTELGRGFA WLDMGTHSSL LQAGQYVQOLL EQRQGVRISC
5
251 VEEIALRMGY ISARQCHELG RELESSSYGR YLMDVAETLM SGPA

Figure 11

5 1 MRLLVTGGAG FIGSHFVRQL LAGAYPDLAG ARTVVVDKLT YAGNLANLDP
5 51 VADHPSLEFV HADIRDAEVN SRVVRGADV VHFAAESHVD RSIADASAFV
0 101 ETNVRGTQVL LQAAVEAGAG RFVHVSTDEV YGSIAEGSWR EEQPLAPNSP
0 151 YAASKAASDL LALAYHRTYG LPVVVTRCSN NYGPYQHPEK VVPLFATNLL
5 201 DGLTVPLYSD GGNSRDWLHV DDHCRGISLV ATRGRPGEVY HIGGGTELTN
5 251 RELTKRLLGL CGADASSVRH VADRPGHDLR YALDIGKITG ELGYAPRTDF
301 TTGLADTVRW YAENRAWWEP LKKAAQEARR TD

)

Figure 12

1 VSTPSAPPVP GAPSPAGHPD EGLWVRRYRP VRDPELRLVC FPHAGGAATS
5 FAALARGLDE TVEALAVQYP GRQDRRHEPF IPSISGLVDQ VVPEILRWAD
10 RPLALFGHSM GATVAFEVAR RL RGSGQASP VHLLVSGRRA PTVRRRDVAH
15 LLDDDALIAE IATLQGTEDA VLQDEELLRL ALPAIRNDYR AAGTYAYVPG
20 GALDCPVTVL TGDRDPDVPL EEARAWRELT TGPFALHTFA GGHFYLNDRM
25 DEVCRTIGDA LAGTATADTA TGTVPVRTAA DTSTGPVPPR TAADTAREPV
30 PPRSAPAPHG AARRRADAVR PGDPVDTARR VLVSARTADS AVTPFDGISG
35 WLAERLRAGR FDVSRVFVFAE LRGWSFHPGT GNLHHASGRF FSVEGLHVRT
40 DRLPERGWTQ PIIVQPEVGL LGIVAREIDG VLHFLMQAKM EPGNVNVLQV
45 SPTVQATRSN FTGVHGRDI RYLDLFMGPR RARVLVDSIQ SEQADWFLAK
50 RNRNMIVELA ADDDLDIGED FRWLTLGQLR RLLMLDNVVN MDARSILACL
55 PTADADASAP SPVLRSSFFGS PGAARHTTAE VLTWFTGVRA LRELVQNRVP
60 LDTVTADGWY RTPHEIAHES GRHFRVMAAE VSASSREVTS WTQPLIEPRL
65 PGLMALLVKS VDGVLHALVR ARVDVGHLNV AELAPTVQCR PQEHTGPRGL
70 PGPPYLEDVL SAPPQDVRYD AVQSEEGGRF FHAQNRYVIV EVPHDFPEDA
75 PDDFAWLSLG QLTGLLAHGN YLNIELRTLV ACAHTLY

35

40

Figure 13

5 1 MVNDPMPRGS GSGSVVVLGG AGYVGRHVCA AFAARGRDVV VVGRRPPEEP
51 51 MPYRCVTLDL AGTDPAALAA ALDAERPDTI VNSVGSIWGR TDEQMWSATA
0 101 VPTLRLLEAL ALMSARPRLV HLGSVLEYGP VTPGGSVGAD AVPRPDTAYG
0 151 RSKLAASEAV LRGTSGGWVD GVVLRVSNVS GPGTPRISLL GQVAERLLAA
5 201 AGTGAEAVVE LSRLRAHRDY DVDRVADAV VAAARAPAVP VAVGIGRGEA
5 251 VAVRDLVGLF IEASGIPARV VERPAPGRAP GHREDWLRVD TGAARALLGW
301 301 APRRSLSLRESV RDCWHDLVRA HRLPTTPSKH SGG

Figure 14

5 1 VTTYVWDYLA EYQNERADLL DAVETVFASG QLVLGPSVDG FEKEFADYHG
51 51 LRHCGGVVDNG TNAVKLGLQA LGVPGPGDEVV TVSNTAAAPTV VAIDGTGATP
10 101 VFVDVRAEDH LMDDTDQVADV ITPTKALLP VHLYGQCVDM APLRALAEQH
15 151 GLVVLEDCAQ AHGARHHGEL AGTLGDAAAAF SFYPTKVLGA YGDGGAVLTD
20 201 DADVDRALRR LRYYGMEDVY YVVQTPGHNS RLDEVQAEIL RRKILTRLDYR
25 251 IEGRRRAVARR YAEGLANLTG PGGLVLPSVT EGNDHVYYVY VVRHPRRDDI
30 301 IEALKSYGIS LNISYPWPVH TMTGFAHLGY AKGSLPVTER LADEIFSLPM
20 351 YPGLAPDVQD KVIAALHEVL ATL

20

25

Figure 15

5 1 VSPAPATEDP AAAGRRLQLT RAAQWFAGTQ DDPYALVLRA EATDPAPYEE
 51 RIRAHGPLFR SDLLDTWVTA SRAVADEVIT SPAFDGLTAD GRRPGARELP
10 101 LSGTALDADR ATCARFGALT AWGGPLLPAP HERALRESAE RRAHTLLDGA
 151 EAALAADGTV DLVDAYARRL PALVLREQLG VPEEAATAFE DALAGCRRTL
20 201 DGALCPQLLP DAVAGVRAEA ALTAVLASAL RGTPAGRDPD AVAAARTLAV
 251 AAAEPAATLV GNAVQELLAR PAQWAELVRD PRLAAAATVE TLRVAPPVRL
 301 ERRVARED TD IAGQRLPAGG SVVILVAAVN RAPVSAGSDA STTVPHAGGR
 351 PRTSAPSVP S APFDLTRPV A PGPFGLPGD LHFRLLGGPLV GTVAEEAALGA
25 401 LAARLPGLRA AGPAVRRRS PVLHGHARLP VAVARTARDL PATA PRN

Figure 16

5 1 MRILLTSFAH NTHYYNLVPL GWALRAAGHD VRVASQPSLT GTITGSLTA
51 51 VPVGDDTAIV ELITEIGDDL VLYQQGMDFV DTRDEPLSWE HALGQQTIMS
10 101 AMCFSPNGD STIDDMVALA RSWKPDVLW EPFTYAGPVA AHACGAAHAR
15 151 LLWGPDVVLN ARRQFTRLA ERPVEQREDP VGEWLTWTLE RHGLAADADT
20 201 IEELFAGQWT IDPSAGSLRL PVDGEVVPMR FVPYNGASVV PAWLSEPPAR
25 251 PRVCVTLGVS TRETYGTDGV PFHELLAGLA DVDAEIVATL DAGQLPDAAG
30 301 LPGNVRVVDF VPLDALLPSC AAIVHHGGAG TCFTATVHGV PQIVVASLWD
35 351 APLKAHQLAE AGAGIALDPG ELGVDTLRGA VVRVLESREM AVAARRLADE
20 401 MLAAPTPAAL VPRLERLTAH HRRA

Figure 17

5 1 MNLEYSGDIA RLYDLVHQGK GKDYRAEAEELAALVTQRRP GARSLLDVAC
51 51 GTGMHLRHLG DLFEEVAGVE MSPDMLAIAQ RRNPEAGIHR GDMRDFALGR
10 101 RFDAVICMFS SIGHMRDQRE LDAAIGRFAA HLPSGGVVIV DPWWFPETFT
15 151 PGYVGASLVE AEGRTIARFS HSALEDGATR IDVDYLVGVP GEGVRHLKET
201 201 HRITLFGRAQ YEAAFTAAGM SVEYLPHAAT DRGLFVGVQA

15